

RESULT	2	CHKESTFLUA			
LOCUS		1383 bp	mRNA	VRT	12-DEC-1996
DEFINITION	Chicken mRNA for unknown protein, complete cds.				
ACCESSION	D26311				
NID	g517092				
KEYWORDS	.				
SOURCE	Gallus gallus lens fibers cDNA to mRNA, clone CLFEST4.				
ORGANISM	Gallus gallus				
	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.				
REFERENCE	1 (sites)				
AUTHORS	Sawada,K., Agata,K. and Eguchi,G.				
TITLE	Characterization of terminally differentiated cell state by categorizing cDNA clones derived from chicken lens fibers				
JOURNAL	Int. J. Dev. Biol. 40 (3), 531-535 (1996)				
MEDLINE	96437509				
REFERENCE	2 (bases 1 to 1383)				
AUTHORS	Sawada,K., Agata,K. and Eguchi,G.				
TITLE	Analysis of the cDNA library of chicken lens fibers: identification of a cDNA coding a novel leucine zipper protein which has constructive similarities with the CREB family				
JOURNAL	Unpublished (1994)				
REFERENCE	3 (bases 1 to 1383)				
AUTHORS	Sawada,K.				
TITLE	Direct Submission				
JOURNAL	Submitted (25-DEC-1993) to the DDBJ/EMBL/GenBank databases. Kaichiro Sawada, Biohistory Research Hall; 1-1 Murasaki-cho, Takatsuki, Osaka 569-11, Japan (E-mail:Kaichiro.Sawada@ims.brh.co.jp, Tel:0726-81-9754, Fax:0726-81-9757)				
FEATURES	Location/Qualifiers				
source	1. .1383 /organism="Gallus gallus" /db_xref="taxon:9031" /clone="CLFEST4" /tissue_type="lens fibers"				
CDS	36. .1088 /codon_start=1 /product="unknown protein" /db_xref="PID:d1005915" /db_xref="PID:g517093" /translation="MRRGEGPAPRRRWLLLLAVLAALCCAAAGSGGRRRAASLGEMLR EVEALMEDTQHKLRNAVQEMEAE EEGAKKLSEVN FENLPPTYHNESNTETRIGNKT VQ THQ EIDKVT DNR TGST I FSET I I TSIKGGENKRNHECI I DEDCETGKYCQFSTFEYKC QPC KTQH THCSRDVECCGDQLCVWGECRKATSRGENGTICENQHDCNPGTCCAFQKEL LFPVCTPLPEEGEPCHDPSNRLLNLITWELEPDGVLERPCASGLICQPQSSHSTTSV CELSNNETRKNEKEDPLNMDEMPFISLIPRDI LSYDEESSVIQEV RKELESLEDQAGV KSEHDP AHDLFLGDEI"				
polyA_site	1383				
BASE COUNT	414 a	306 c	352 g	311 t	
ORIGIN					

Query Match 28.0%; Score 294; DB 17; Length 1383;
Best Local Similarity 71.0%; Pred. No. 1.67e-195;
Matches 497; Conservative 0; Mismatches 203; Indels 0; Gaps 0;

Db	143	GGCCAGCCCTGGGCGAGATGCTGCGGGAGGTTGAGGCGCTGATGGAGGACACGCAGCACAA	202
Qy	132	GGCCACCCTCAATGAGATGTTCCGCGAGGTTGAGGAACTGATGGAGGACACGCAGCACAA	191
Db	203	GCTGCGCAACGCGGTGCAGGAGATGGAAGCTGAAGAAGAAGGGGCAAAAAAACTGTCAGA	262
Qy	192	ATTGCGCAGCGCGTGAAGAGATGGAGGCAGAAGAAGCTGCTGCTAAAGCATCATCAGA	251
Db	263	AGTAAACTTTGAAACTTACCTCCCACCTACCATAATGAGTCCAACACAGAAACCAGAAT	322
Qy	252	AGTGAACCTGGCAAACCTTACCTCCCAGCTATCACAAATGAGACCAACACAGACACGAACGT	311
Db	323	TGGTAATAAAACTGTTTCACTCATCAAGAAATTGATAAGGTTACAGATAACAGAACTGG	382
Qy	312	TGGAATAATACCATCCATGTGCACCGAGAATTCACAAGATAACCAACAACCGAGCTGG	371

Db	383	ATCAACAATTTTTCCGAGACAATTATTACATCTATAAAGGGTGGAGAAAACAAAGAAA	442
Qy	372	ACAAATGGTCTTTTCAGAGACAGTTATCACATCTGTGGGAGACGAAGAAGGCAGAAGGAG	431
Db	443	TCATGAGTGTATCATTGATGAAGACTGTGAAACAGGAAAGTATTGCCAGTTCTCCACCTT	502
Qy	432	CCACGAGTGCATCATCGACGAGGACTGTGGGCCAGCATGTACTGCCAGTTTGCCAGCTT	491
Db	503	TGAATACAAGTGTGAGCCCTGTAAAACCCAGCATACACACTGCTCACGAGATGTTGAATG	562
Qy	492	CCAGTACACCTGCCAGCCATGCCGGGGCCAGAGGATGCTCTGCACCCGGGACAGTGAGTG	551
Db	563	CTGCGGAGACCAGCTTTGTGTTTGGGGTGAGTGCAGGAAAGCCACTTCAAGAGGAGAAAA	622
Qy	552	CTGTGGAGACCAGCTGTGTGTCTGGGGTCACTGCACCAAATGGCCACCAGGGGCAGCAA	611
Db	623	TGGTACCAATTGTGAGAACCAACATGACTGCAACCAGGAACGTGCTGTGCTTTTCAGAA	682
Qy	612	TGGGACCATCTGTGACAACCAGAGGGGACTGCCAGCCGGGGCTGTGCTGTGCCTTCCAGAG	671
Db	683	AGAACTGCTGTTTCTGTGTGCACTCCGTTACCCGAAGAAGGTGAACCTTGCCATGATCC	742
Qy	672	AGGCCTGCTGTTCCCTGTGTGCACACCCCTGCCCGTGGAGGGCGAGCTTTGCCATGACCC	731
Db	743	TTCAAACAGACTTCTCAACCTGATCACCTGGGAACCTGGAACCTGATGGAGTACTAGAGCG	802
Qy	732	CGCCAGCCGGCTTCTGGACCTCATCACCTGGGAGCTAGAGCCTGATGGAGCCTTGGACCG	791
Db	803	CTGCCCATGTGCAAGTGGCTTGATCTGCCAACCTCAGAGC	842
Qy	792	ATGCCCTTGTGCCAGTGGCCTCCTTGCCAGCCCCACAGC	831